



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/042,526
Source: o/p
Date Processed by STIC: 8-4-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby,
Room 1B03, Arlington, VA 22202

Revised 05/17/04



OIKE

RAW SEQUENCE LISTING

DATE: 08/04/2004

PATENT APPLICATION: US/10/042,526

TIME: 10:04:39

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\08042004\J042526.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

E--> 6 (i) APPLICANT: *mandatory response needed*

8 (ii) TITLE OF INVENTION: Papilloma Virus Capsomere Vaccine Formulations

9 and Methods of Use

E--> 11 (iii) NUMBER OF SEQUENCES: 27 *28 see pg. 5*

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

15 (B) STREET: 233 South Wacker Drive, 6300 Sears Tower

16 (C) CITY: Chicago

17 (D) STATE: Illinois

18 (E) COUNTRY: United States of America

19 (F) ZIP: 60606-6402

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/10/042,526

C--> 29 (B) FILING DATE: 29-Apr-2002

30 (C) CLASSIFICATION:

32 (viii) ATTORNEY/AGENT INFORMATION:

33 (A) NAME: Williams Jr., Joseph A.

34 (B) REGISTRATION NUMBER: 38,659

35 (C) REFERENCE/DOCKET NUMBER: 27013/34028

37 (ix) TELECOMMUNICATION INFORMATION:

38 (A) TELEPHONE: 312-474-6300

39 (B) TELEFAX: 312-474-0448

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

185 (2) INFORMATION FOR SEQ ID NO: 2:

187 (i) SEQUENCE CHARACTERISTICS:

188 (A) LENGTH: 506 amino acids *505 see p. 3*

189 (B) TYPE: amino acid

190 (D) TOPOLOGY: linear

192 (ii) MOLECULE TYPE: protein

194 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

196 Met Ser Leu Trp Leu Pro Ser Glu Ala Thr Val Tyr Leu Pro Pro Val

197 1 5 10 15

199 Pro Val Ser Lys Val Val Ser Thr Asp Glu Tyr Val Ala Arg Thr Asn

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Input Set : A:\pto.lm.txt

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```

200          20          25          30
202 Ile Tyr Tyr His Ala Gly Thr Ser Arg Leu Leu Ala Val Gly His Pro.
203          35          40          45
205 Tyr Phe Pro Ile Lys Lys Pro Asn Asn Asn Lys Ile Leu Val Pro Lys
206          50          55          60
208 Val Ser Gly Leu Gln Tyr Arg Val Phe Arg Ile His Leu Pro Asp Pro
209 65          70          75          80
211 Asn Lys Phe Gly Phe Pro Asp Thr Ser Phe Tyr Asn Pro Asp Thr Gln
212          85          90          95
214 Arg Leu Val Trp Ala Cys Val Gly Val Glu Val Gly Arg Gly Gln Pro
215          100          105          110
217 Leu Gly Val Gly Ile Ser Gly His Pro Leu Leu Asn Lys Leu Asp Asp
218          115          120          125
220 Thr Glu Asn Ala Ser Ala Tyr Ala Ala Asn Ala Gly Val Asp Asn Arg
221          130          135          140
223 Glu Cys Ile Ser Met Asp Tyr Lys Gln Thr Gln Leu Cys Leu Ile Gly
224 145          150          155          160
226 Cys Lys Pro Pro Ile Gly Glu His Trp Gly Lys Gly Ser Pro Cys Thr
227          165          170          175
229 Asn Val Ala Val Asn Pro Gly Asp Cys Pro Pro Leu Glu Leu Ile Asn
230          180          185          190
232 Thr Val Ile Gln Asp Gly Asp Met Val Asp Thr Gly Phe Gly Ala Met
233          195          200          205
235 Asp Phe Thr Thr Leu Gln Ala Asn Lys Ser Glu Val Pro Leu Asp Ile
236          210          215          220
238 Cys Thr Ser Ile Cys Lys Tyr Pro Asp Tyr Ile Lys Met Val Ser Glu
239 225          230          235          240
241 Pro Tyr Gly Asp Ser Leu Phe Phe Tyr Leu Arg Arg Glu Gln Met Phe
242          245          250          255
244 Val Arg His Leu Phe Asn Arg Ala Gly Ala Val Gly Glu Asn Val Pro
245          260          265          270
247 Asp Asp Leu Tyr Ile Lys Gly Ser Gly Ser Thr Ala Asn Leu Ala Ser
248          275          280          285
250 Ser Asn Tyr Phe Pro Thr Pro Ser Gly Ser Met Val Thr Ser Asp Ala
251          290          295          300
255 Gln Ile Phe Asn Lys Pro Tyr Trp Leu Gln Arg Ala Gln Gly His Asn
256 305          310          315          320
258 Asn Gly Ile Cys Trp Gly Asn Gln Leu Phe Val Thr Val Val Asp Thr
259          325          330          335
261 Thr Arg Ser Thr Asn Met Ser Leu Cys Ala Ala Ile Ser Thr Ser Glu
262          340          345          350
264 Thr Thr Tyr Lys Asn Thr Asn Phe Lys Glu Tyr Leu Arg His Gly Glu
265          355          360          365
267 Glu Tyr Asp Leu Gln Phe Ile Phe Gln Leu Cys Lys Ile Thr Leu Thr
268          370          375          380
270 Ala Asp Val Met Thr Tyr Ile His Ser Met Asn Ser Thr Ile Leu Glu
271 385          390          395          400
273 Asp Trp Asn Phe Gly Leu Gln Pro Pro Pro Gly Gly Thr Leu Glu Asp.
274          405          410          415

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```

276 Thr Tyr Arg Phe Val Thr Ser Gln Ala Ile Ala Cys Gln Lys His Thr
277           420           425           430
279 Pro Pro Ala Pro Lys Glu Asp Pro Leu Lys Lys Tyr Thr Phe Trp Glu
280           435           440           445
282 Val Asn Leu Lys Glu Lys Phe Ser Ala Asp Leu Asp Gln Phe Pro Leu
283           450           455           460
285 Gly Arg Lys Phe Leu Leu Gln Ala Gly Leu Lys Ala Lys Pro Lys Phe
286 465           470           475           480
288 Thr Leu Gly Lys Arg Lys Ala Thr Pro Thr Thr Ser Ser Thr Ser Thr
289           485           490           495
E--> 291 Thr Ala Lys Arg Lys Lys Arg Lys Leu * delete, do not count
292           500           505 stop codon
338 (2) INFORMATION FOR SEQ ID NO: 4:
340 (i) SEQUENCE CHARACTERISTICS:
341 (A) LENGTH: 98 amino acids 97 (same)
342 (B) TYPE: amino acid error
343 (D) TOPOLOGY: linear
345 (ii) MOLECULE TYPE: protein
347 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
349 Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln
350 1           5           10           15
352 Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser
353           20           25           30
355 Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp
356           35           40           45
359 Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr
360           50           55           60
363 Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu
364 65           70           75           80
366 Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln
367           85           90           95
E--> 369 Lys Pro * delete
583 (2) INFORMATION FOR SEQ ID NO: 18:
585 (i) SEQUENCE CHARACTERISTICS:
586 (A) LENGTH: 97 amino acids 96
587 (B) TYPE: amino acid
588 (D) TOPOLOGY: linear
590 (ii) MOLECULE TYPE: protein
592 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:
594 Met Ser Leu Leu Thr Glu Val Glu Thr Leu Thr Arg Asn Gly Trp Glu
595 1           5           10           15
597 Cys Lys Cys Ser Asp Ser Ser Asp Pro Leu Ile Ile Ala Ala Ser Ile
598           20           25           30
601 Ile Gly Ile Leu His Leu Ile Leu Trp Ile Phe Tyr Arg Leu Phe Phe
602           35           40           45
604 Lys Cys Ile Tyr Arg Arg Leu Lys Tyr Gly Leu Lys Arg Gly Pro Ser
605           50           55           60
607 Thr Glu Gly Ala Pro Glu Ser Met Arg Glu Glu Tyr Arg Gln Glu Gln
608 65           70           75           80

```

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610 Gln Ser Ala Val Asp Val Asp Asp Val His Phe Val Asn Ile Glu Leu
611 85 90 95

E--> 613 Glu ^⑦
delete.

(2) INFORMATION FOR SEQ ID NO:28: → last seq. in submitted file.

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CATCTGAAGC TTATTGTACG CACAACCGAA GCGTAGAGTC ACACTTG

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VERIFICATION SUMMARY

DATE: 08/04/2004

PATENT APPLICATION: US/10/042,526

TIME: 10:04:40

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\08042004\J042526.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:6 M:200 E: Mandatory Header Field missing, [(i) APPLICANT:] of (1) Value not provided
L:291 M:342 E: Invalid Stop Code On Error, STOP CODON:*
L:303 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:369 M:342 E: Invalid Stop Code On Error, STOP CODON:*
L:369 M:203 E: No. of Seq. differs, LENGTH:Input:98 Found:99 SEQ:4
L:379 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5
L:393 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6
L:407 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:421 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8
L:436 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9
L:450 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10
L:464 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11
L:478 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=12
L:492 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13
L:506 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14
L:520 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15
L:534 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=16
L:548 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=17
L:613 M:342 E: Invalid Stop Code On Error, STOP CODON:*
L:613 M:203 E: No. of Seq. differs, LENGTH:Input:97 Found:98 SEQ:18
L:623 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=19
L:637 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=20
L:651 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=21
L:665 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=22
L:679 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=23
L:693 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24
L:707 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25
L:721 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26
L:735 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27
L:751 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=28
L:11 M:203 E: No. of Seq. differs, : Input 27, Counted 28